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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/751,708A

DATE: 11/06/2002 P.6
TIME: 14:14:20

Input Set : A:\751708.txt

Output Set: N:\CRF4\11062002\I751708A.raw

3 <110> APPLICANT: Terman, David S
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
7 <130> FILE REFERENCE: 751708
9 <140> CURRENT APPLICATION NUMBER: US 09/751,708A
C--> 10 <141> CURRENT FILING DATE: 2002-10-15
12 <150> PRIOR APPLICATION NUMBER: US 60/173,371
13 <151> PRIOR FILING DATE: 1999-12-28
15 <160> NUMBER OF SEQ ID NOS: 166
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 801
21 <212> TYPE: DNA
22 <213> ORGANISM: Staphylococcus sp.
24 <400> SEQUENCE: 1
25 atgtataaga gattatattat ttcacatgta attttgatat tcgcactgat attagttatt 60
27 tctacaccca acgttttagc agagagtcaa ccagatccta aaccagatga gttgcacaaa 120
29 tcgagtaaata tcaactgggtt gatggaaaat atgaaagtgt tgtatgatga taatcatgta 180
31 tcagcaataa acgttaaatc tatagatcaa tttctatact ttgacttaat atattctatt 240
33 aaggacacta agttagggaa ttatgataat gttcgagtcg aatttaaaaa caaagattta 300
35 gctgataaat acaaagataa atacgtagat gtgtttggag ctaattatta ttatcaatgt 360
37 tatttttcta aaaaaacgaa tgatattaat tcgcatcaaa ctgacaaaacg aaaaacttgt 420
39 atgtatgggtg gtgtaactga gcataatgga aaccaattag ataaatatag aagtattact 480
41 gttcgggtat ttgaagatgg taaaaattta ttatcttttg acgtacaaac taataagaaa 540
43 aaggtgactg ctcaagaatt agattaccta actcgtcact atttggtgaa aaataaaaaa 600
45 ctctatgaat ttaacaactc gccttatgaa acgggatata ttaaatttat agaaaatgag 660
47 aatagctttt ggtatgacat gatgcctgca ccaggagata aatttgacca atctaaatat 720
49 ttaatgatgt acaatgacaa taaaatggtt gattctaaag atgtgaagat tgaagtttat 780
51 cttacgacaa agaaaaagtg a 801
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 886
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic Sequence
62 <400> SEQUENCE: 2
63 cggctcacag cgcgcccggtc tattctcgca ggatcagtcg acatgtataa gagattattt 60
65 atttcacatg taattttgat attcgcactg atattagtta tttctacacc caacgtttta 120
67 gcagagagtc aaccagatcc taaaccagat gagttgcaca aatcgagtaa attcactggt 180
69 ttgatggaaa atatgaaagt tttgtatgat gataatcatg tatcagcaat aaacgttaaa 240
71 tctatagatc aatttctata ctttgactta atatattcta ttaaggacac taagttaggg 300
73 aattatgata atgttcgagt cgaattttaa aacaaagatt tagctgataa atacaaagat 360
75 aaatacgtag atgtgttttg agctaattat tattatcaat gttatttttc taaaaaacg 420
77 aatgatatta attcgcacat aactgacaaa cgaaaaactt gtatgtatgg tgggtgtaact 480

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79 gagcataatg gaaaccaatt agataaatat agaagtatta ctgttcgggt atttgaagat      540
81 ggtaaaaatt tattatcttt tgacgtacaa actaataaga aaaagggtgac tgctcaagaa      600
83 ttagattacc taactcgtca ctatttggtg aaaaataaaa aactctatga atttaacaac      660
85 tcgccttatg aaacgggata tattaaattt atagaaaatg agaatagctt ttggtatgac      720
87 atgatgcctg caccaggaga taaatttgac caatctaaat atttaatgat gtacaatgac      780
89 aataaaatgg ttgattctaa agatgtgaag attgaagttt atcttacgac aaagaaaaag      840
91 tgaggatcca gacatgataa gataccttga tgagtttgga caaacc                      886
94 <210> SEQ ID NO: 3
95 <211> LENGTH: 24
96 <212> TYPE: DNA
97 <213> ORGANISM: Unknown
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Primer
102 <400> SEQUENCE: 3
103 ggcgtcgaca tgtataagag atta                                          24
106 <210> SEQ ID NO: 4
107 <211> LENGTH: 24
108 <212> TYPE: DNA
109 <213> ORGANISM: Unknown
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Primer
114 <400> SEQUENCE: 4
115 gccggatcct cactttttct ttgt                                          24
118 <210> SEQ ID NO: 5
119 <211> LENGTH: 22
120 <212> TYPE: DNA
121 <213> ORGANISM: Unknown
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Primer
126 <400> SEQUENCE: 5
127 tatgaaagtt ttgtatgatg at                                          22
130 <210> SEQ ID NO: 6
131 <211> LENGTH: 20
132 <212> TYPE: DNA
133 <213> ORGANISM: Unknown
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Primer
138 <400> SEQUENCE: 6
139 agtgacgagt taggtaatct                                          20
142 <210> SEQ ID NO: 7
143 <211> LENGTH: 1443
144 <212> TYPE: DNA
145 <213> ORGANISM: Staphylococcus aureus
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (262)..(1032)
150 <223> OTHER INFORMATION:
W--> 152 <400> 7
153 ccaaaataat ggcaagtact ccgttgtcaa taccaagtaa gtaagatc tgaaatgtat      60

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155 aatagagtaa aaatgaaatc tttttattat attatagaca agtataaaaa aggtatagta 120
157 atatatgtat gtataagtaa ataatagataa ttctataatt attgtatata actaataatt 180
159 acttcgacaa aaataatcta ttatccaaat atttttagata ataaaaagtt tgtatggaat 240
161 tatgcttttag aggtgagcaa a atg aaa aaa aca gca ttt ata cta ctt tta 291
162                               Met Lys Lys Thr Ala Phe Ile Leu Leu Leu
163                               1                               5                               10
165 ttc att gcc cta acg tgg aca aca agt cca ctt gta aat ggt agc gag 339
166 Phe Ile Ala Leu Thr Trp Thr Thr Ser Pro Leu Val Asn Gly Ser Glu
167                               15                               20                               25
169 aaa agc gaa gaa ata aat gaa aaa gat ttg cga aaa aag tct gaa ttg 387
170 Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu
171                               30                               35                               40
173 cag gga gca gct tta ggc aat ctt aaa caa atc tat tat tac aat gaa 435
174 Gln Gly Ala Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu
175                               45                               50                               55
177 aaa gct aaa act gaa aat aaa gag agt cac gat caa ttt tta cag cat 483
178 Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu Gln His
179                               60                               65                               70
181 act ata ttg ttt aaa ggc ttt ttt aca aat cat tca tgg tat aac gat 531
182 Thr Ile Leu Phe Lys Gly Phe Phe Thr Asn His Ser Trp Tyr Asn Asp
183 75                               80                               85                               90
185 tta tta gta gat ttt gat tca aag gat att gtt gat aaa tat aaa ggg 579
186 Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly
187                               95                               100                               105
189 aaa aaa gta gac tta tat ggt gct tat tat ggt tat caa tgt gcg ggt 627
190 Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly
191                               110                               115                               120
193 ggt aca cca aac aaa aca gct tgc atg tat ggt ggt gta acg tta cat 675
194 Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr Leu His
195                               125                               130                               135
197 gat aat aat cga ttg acc gaa gag aaa aaa gtg ccg atc aat tta tgg 723
198 Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn Leu Trp
199                               140                               145                               150
201 cta gac ggt aaa caa aat aca gta cct ttg gaa acg gtt aaa acg aat 771
202 Leu Asp Gly Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys Thr Asn
203 155                               160                               165                               170
205 aag aaa aat gta act gtt cag gag ttg gat ctt caa gca aga cgt tat 819
206 Lys Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr
207                               175                               180                               185
209 tta cag gaa aaa tat aat tta tat aac tct gat gtt ttt gat ggg aag 867
210 Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys
211                               190                               195                               200
213 gtt cag agg gga tta atc gtg ttt cat act tct aca gaa cct tcg gtt 915
214 Val Gln Arg Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro Ser Val
215                               205                               210                               215
217 aat tac gat tta ttt ggt gct caa gga cag aat tca aat aca cta tta 963
218 Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln Asn Ser Asn Thr Leu Leu
219                               220                               225                               230
221 aga ata tat aga gat aat aaa acg att aac tct gaa aac atg cat att 1011

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222 Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met His Ile
223 235                240                245                250
225 gat ata tat tta tat aca agt taaacatggt agttttgaac acgtaatggt      1062
226 Asp Ile Tyr Leu Tyr Thr Ser
227                255
229 cagattatta tgaaccgaga ataatctgaa agttttacaag cagtaaaaaa agtatatgtg      1122
231 ctataaatatg ctttgagcaa gttggataga tgggtggctat ctgagtataa ggaggtggtg      1182
233 cctatgggtg cttactgaa atcttttagaa aggagacgcc taatgattac aattagttacc      1242
235 aatggttcag tttggtttat tccttattgc attgatagggt ctagtaatca agcttattga      1302
237 attaagcaat aaaaaataac catcgctaac tttggctggt ttcgatgggt aaatggttat      1362
239 taatttaatc tttaatctaa aatagccacc gtctttttaa cgggctcatt agggtaacat      1422
241 gtttgcgcat gttgcccttt t
244 <210> SEQ ID NO: 8
245 <211> LENGTH: 257
246 <212> TYPE: PRT
247 <213> ORGANISM: Staphylococcus aureus
249 <400> SEQUENCE: 8
251 Met Lys Lys Thr Ala Phe Ile Leu Leu Leu Phe Ile Ala Leu Thr Trp
252 1                5                10                15
255 Thr Thr Ser Pro Leu Val Asn Gly Ser Glu Lys Ser Glu Glu Ile Asn
256                20                25                30
259 Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly Ala Ala Leu Gly
260                35                40                45
263 Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
264                50                55                60
267 Lys Glu Ser His Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly
268 65                70                75                80
271 Phe Phe Thr Asn His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp
272                85                90                95
275 Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr
276                100               105               110
279 Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr
280                115               120               125
283 Ala Cys Met Tyr Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr
284                130               135               140
287 Glu Glu Lys Lys Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
288 145               150               155               160
291 Thr Val Pro Leu Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val
292                165               170               175
295 Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn
296                180               185               190
299 Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile
300                195               200               205
303 Val Phe His Thr Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly
304                210               215               220
307 Ala Gln Gly Gln Asn Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn
308 225               230               235               240
311 Lys Thr Ile Asn Ser Glu Asn Met His Ile Asp Ile Tyr Leu Tyr Thr
312                245               250               255

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315 Ser
319 <210> SEQ ID NO: 9
320 <211> LENGTH: 1712
321 <212> TYPE: DNA
322 <213> ORGANISM: Staphylococcus aureus
324 <220> FEATURE:
325 <221> NAME/KEY: CDS
326 <222> LOCATION: (244)..(1044)
327 <223> OTHER INFORMATION:
W--> 329 <400> 9
330 gaactaggta gaaaaataat tatgagaaaa cactatgttg ttaaagatgt ttctgtatat 60
332 aagtttaggt gatgtatagt tacttaattt taaaagcata acttaattaa tataaataac 120
334 atgagattat taaatataat taagtttctt ttaatgtttt tttaattgaa tatttaagat 180
336 tataacatat atttaaagtg tatctagata ctttttgga atgttgata aaggagataa 240
338 aaa atg tat aag aga tta ttt att tca cat gta att ttg ata ttc gca 288
339 Met Tyr Lys Arg Leu Phe Ile Ser His Val Ile Leu Ile Phe Ala
340 1 5 10 15
342 ctg ata tta gtt att tct aca ccc aac gtt tta gca gag agt caa cca 336
343 Leu Ile Leu Val Ile Ser Thr Pro Asn Val Leu Ala Glu Ser Gln Pro
344 20 25 30
346 gat cct aaa cca gat gag ttg cac aaa tcg agt aaa ttc act ggt ttg 384
347 Asp Pro Lys Pro Asp Glu Leu His Lys Ser Ser Lys Phe Thr Gly Leu
348 35 40 45
350 atg gaa aat atg aaa gtt ttg tat gat gat aat cat gta tca gca ata 432
351 Met Glu Asn Met Lys Val Leu Tyr Asp Asp Asn His Val Ser Ala Ile
352 50 55 60
354 aac gtt aaa tct ata gat caa ttt cta tac ttt gac tta ata tat tct 480
355 Asn Val Lys Ser Ile Asp Gln Phe Leu Tyr Phe Asp Leu Ile Tyr Ser
356 65 70 75
358 att aag gac act aag tta ggg aat tat gat aat gtt cga gtc gaa ttt 528
359 Ile Lys Asp Thr Lys Leu Gly Asn Tyr Asp Asn Val Arg Val Glu Phe
360 80 85 90 95
362 aaa aac aaa gat tta gct gat aaa tac aaa gat aaa tac gta gat gtg 576
363 Lys Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys Tyr Val Asp Val
364 100 105 110
366 ttt gga gct aat tat tat tat caa tgt tat ttt tct aaa aaa acg aat 624
367 Phe Gly Ala Asn Tyr Tyr Tyr Gln Cys Tyr Phe Ser Lys Lys Thr Asn
368 115 120 125
370 gat att aat tcg cat caa act gac aaa cga aaa act tgt atg tat ggt 672
371 Asp Ile Asn Ser His Gln Thr Asp Lys Arg Lys Thr Cys Met Tyr Gly
372 130 135 140
374 ggt gta act gag cat aat gga aac caa tta gat aaa tat aga agt att 720
375 Gly Val Thr Glu His Asn Gly Asn Gln Leu Asp Lys Tyr Arg Ser Ile
376 145 150 155
378 act gtt cgg gta ttt gaa gat ggt aaa aat tta tta tct ttt gac gta 768
379 Thr Val Arg Val Phe Glu Asp Gly Lys Asn Leu Leu Ser Phe Asp Val
380 160 165 170 175
382 caa act aat aag aaa aag gtg act gct caa gaa tta gat tac cta act 816
383 Gln Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp Tyr Leu Thr

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:34; Xaa Pos. 2,5,9
Seq#:46; Xaa Pos. 4,6,7
Seq#:53; Xaa Pos. 2,3,6,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25
Seq#:53; Xaa Pos. 26,31,32
Seq#:54; Xaa Pos. 1,6
Seq#:164; Xaa Pos. 3,6

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Input Set : A:\751708.txt
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:152 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:150
L:329 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:327
L:514 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:512
L:679 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:677
L:846 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:844
L:993 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:991
L:1134 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:1132
L:1363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:1361
L:1601 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:1599
L:2170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:2184 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:2182
L:2400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:38,Line#:2398
L:2531 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:40,Line#:2529
L:2926 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:2924
L:3277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:44,Line#:3275
L:3917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:4996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:5000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:16
L:5023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:6205 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:67,Line#:6203
L:6482 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:69,Line#:6480
L:6554 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:71,Line#:6547
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L:6559 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:71,Line#:6557
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L:7029 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:77,Line#:7027
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L:11372 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:105,Line#:11365
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L:12670 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:113,Line#:12668

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Input Set : A:\751708.txt

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L:14204 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:117,Line#:14202
L:14871 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:119,Line#:14869
L:15618 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:121,Line#:15616
L:15739 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:123,Line#:15737
L:16350 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:125,Line#:16348
L:17193 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:127,Line#:17191
L:19628 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:129,Line#:19626
L:22466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:164 after pos.:0